

FIGURE 1

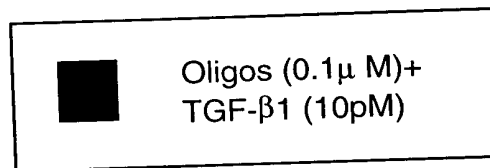
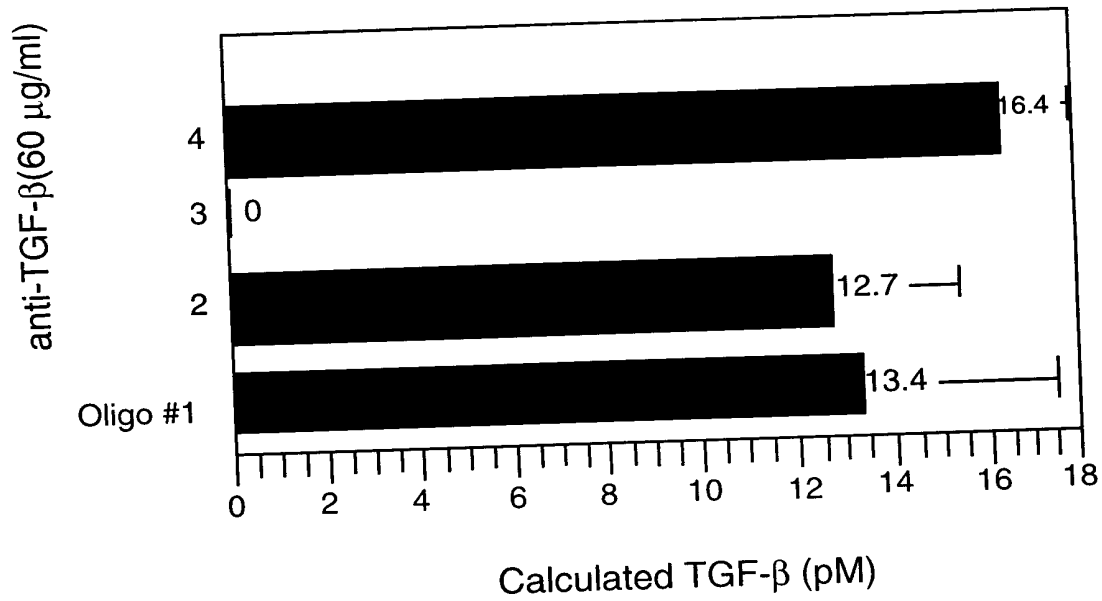
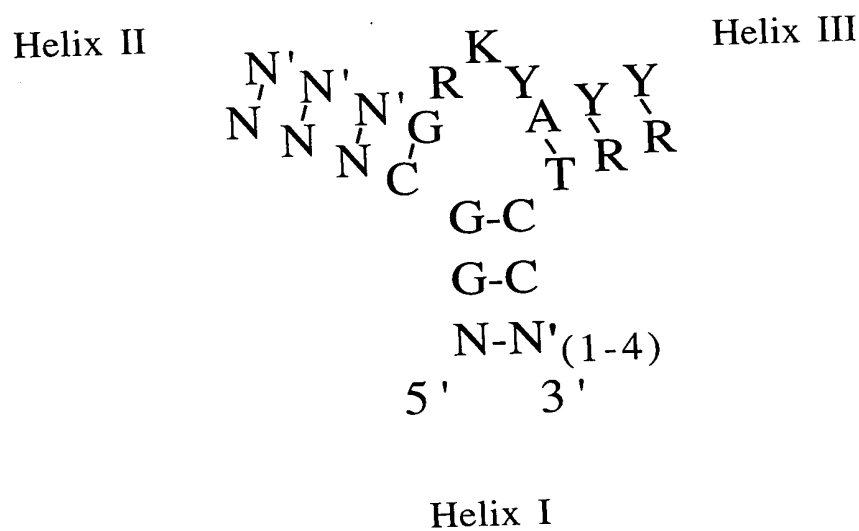


FIGURE 2



SEQ ID NO: 171

FIGURE 3

FIGURE 4

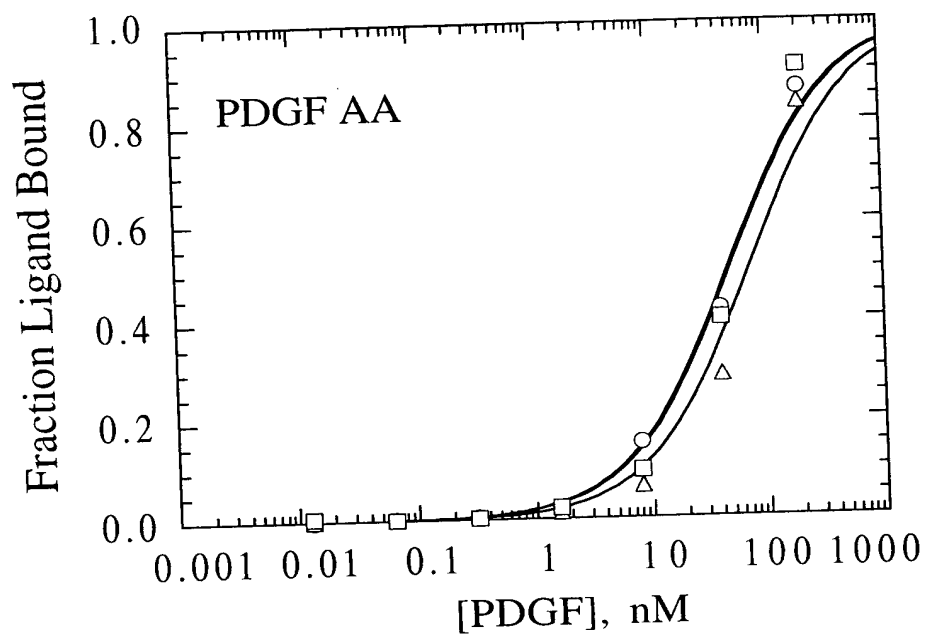


Figure 5A

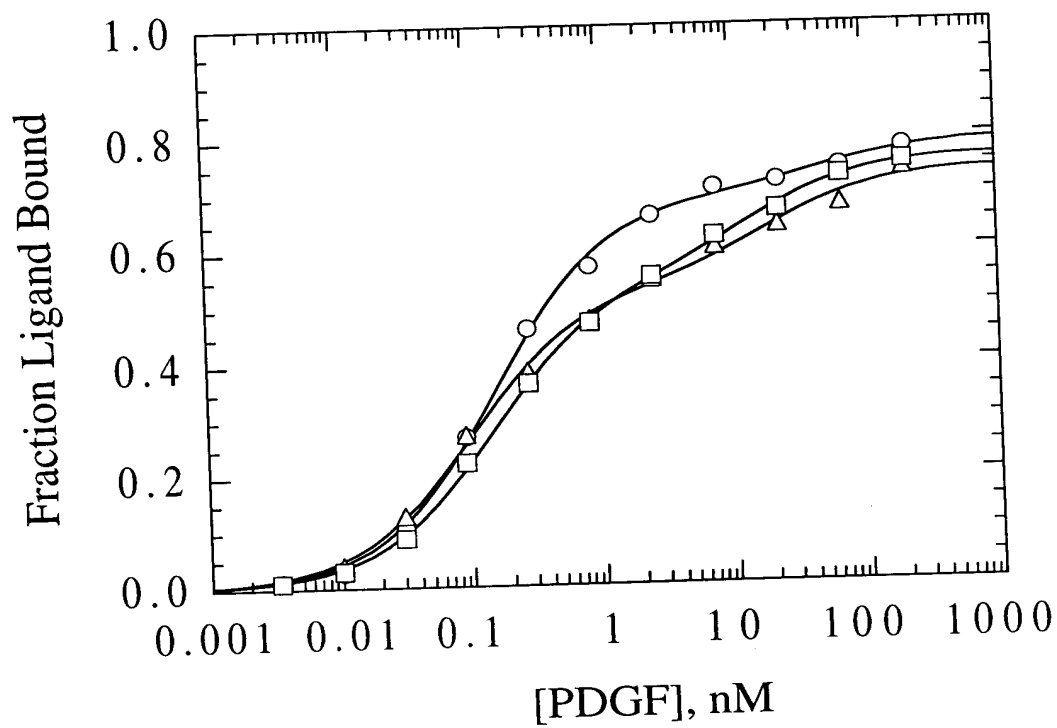


Figure 5B

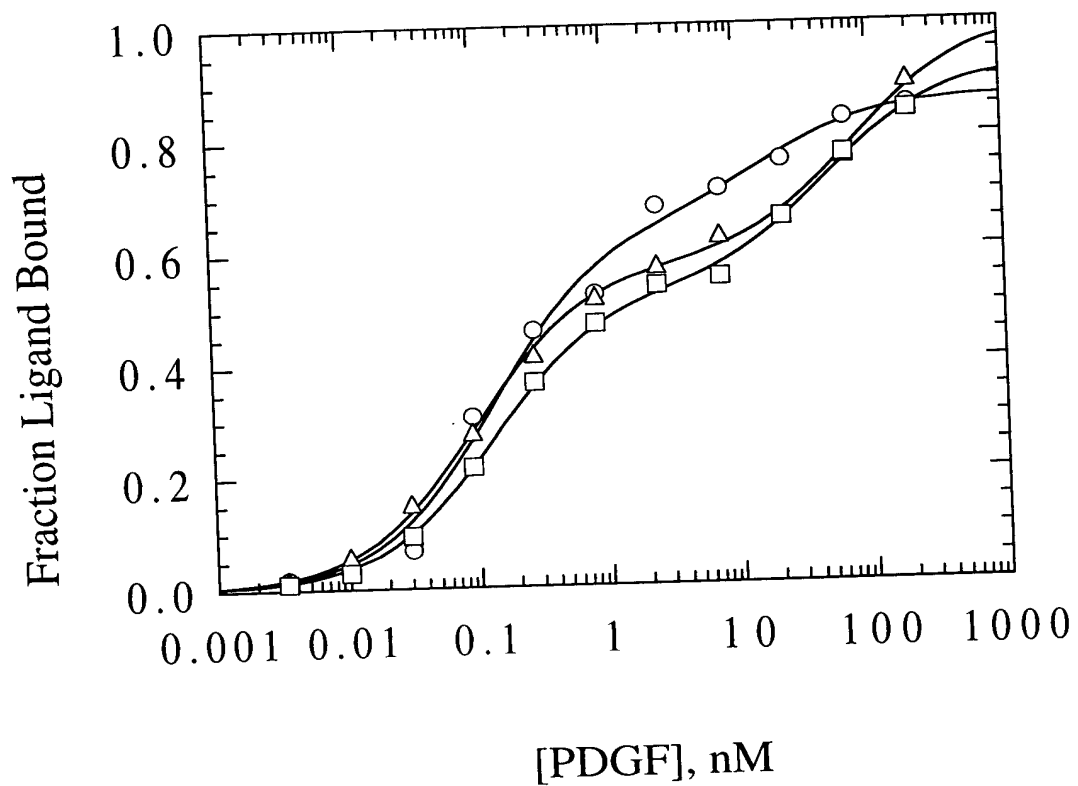


Figure 5C

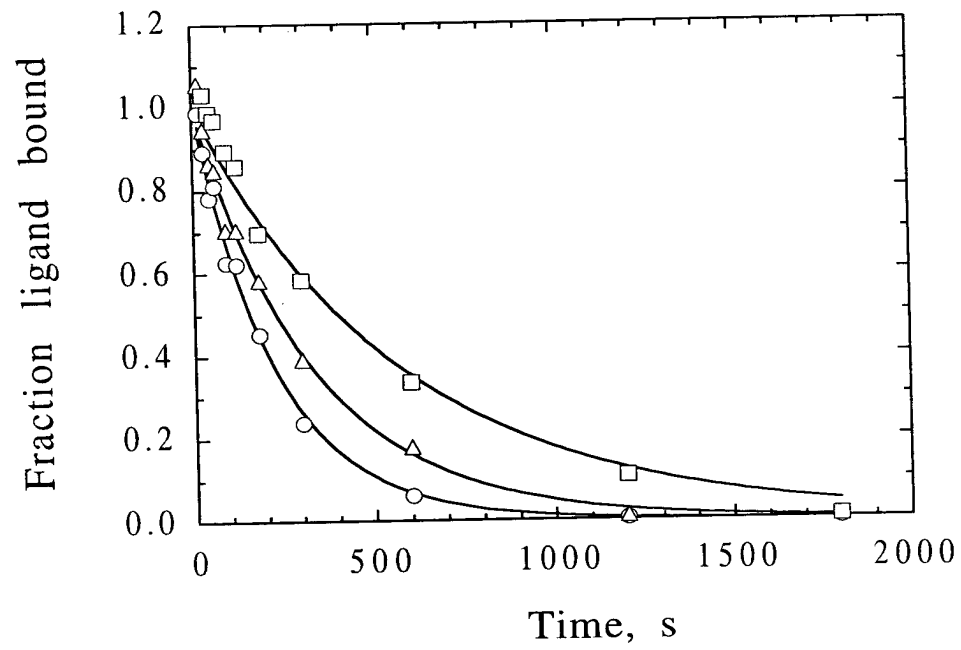


FIGURE 6

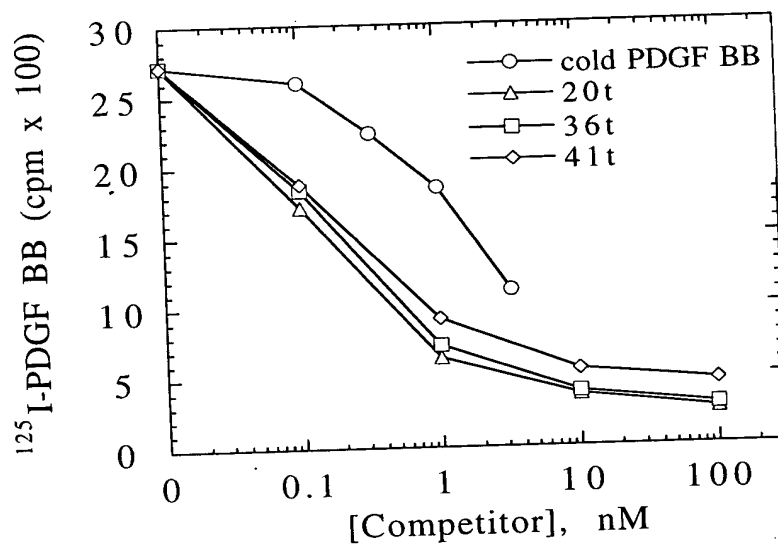


FIGURE 7

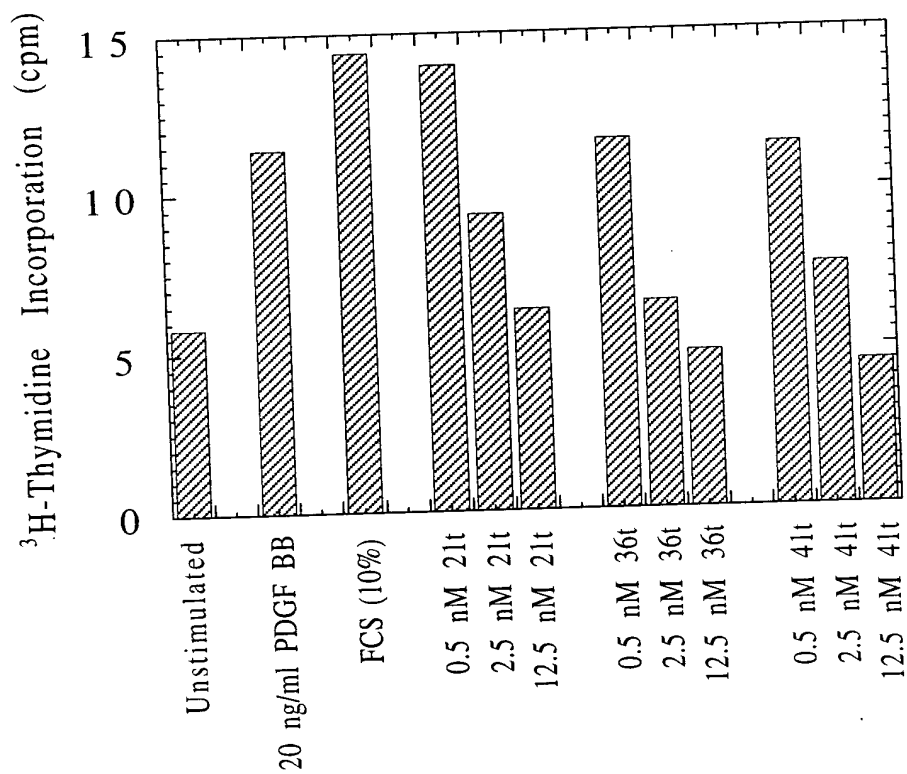
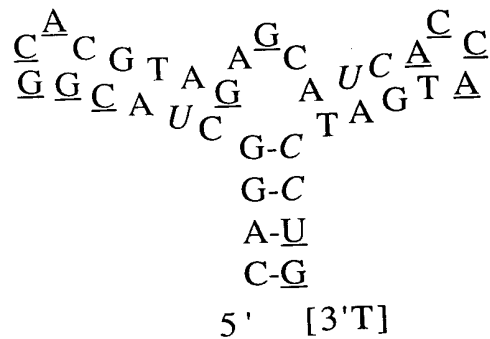
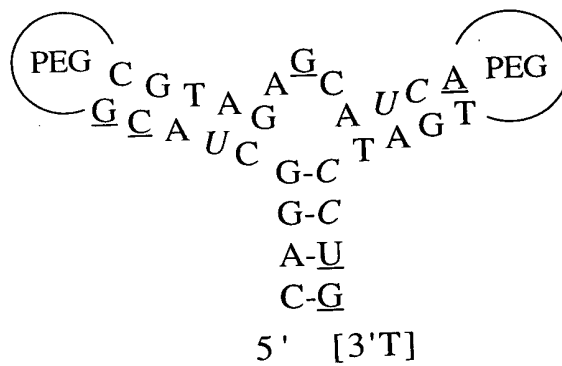


FIGURE 8



$K_d=0.065$ nM

SEQ ID NO: 175



$K_d=0.097$ nM

SEQ ID NO: 176

FIGURE 9

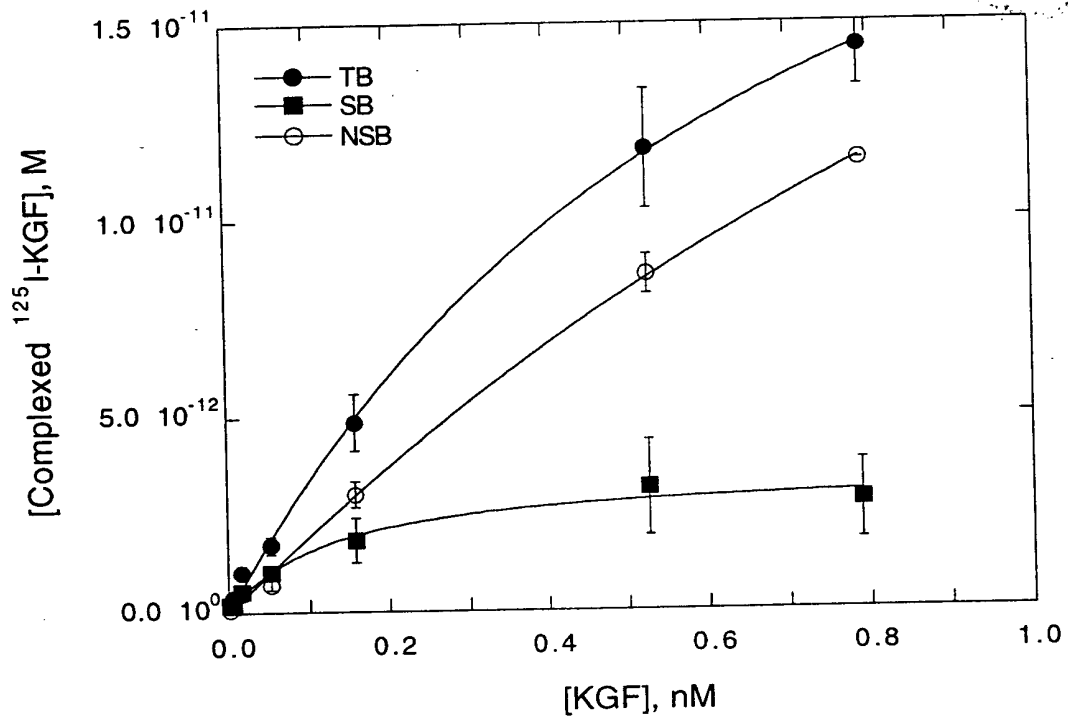


FIGURE 10A

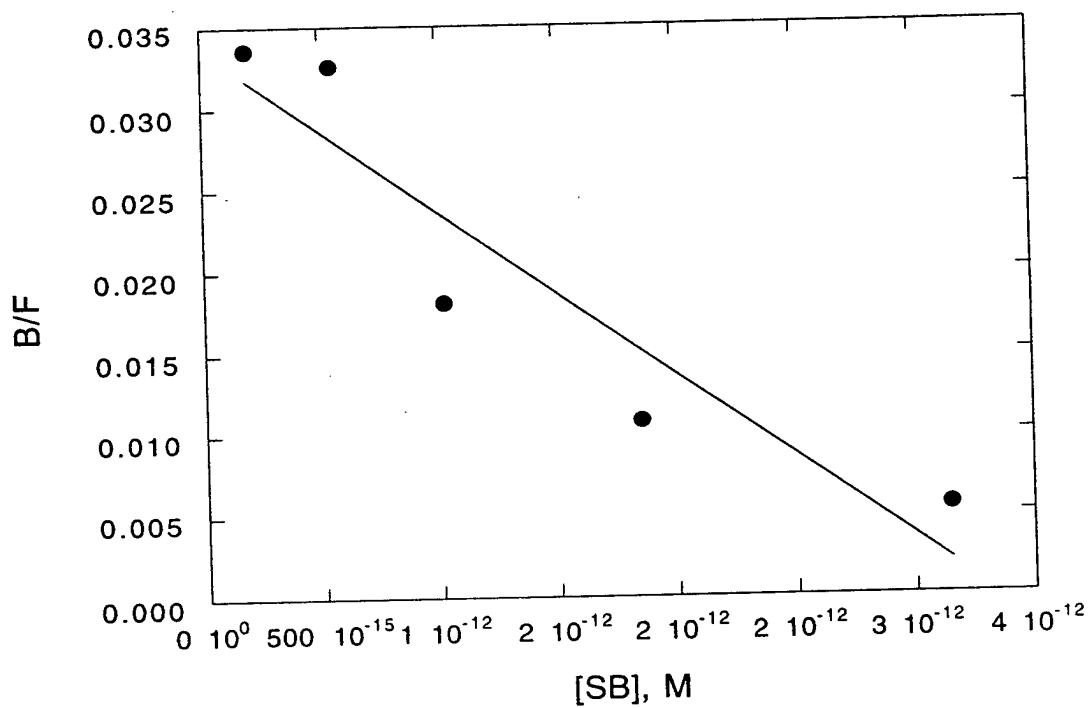


FIGURE 10B

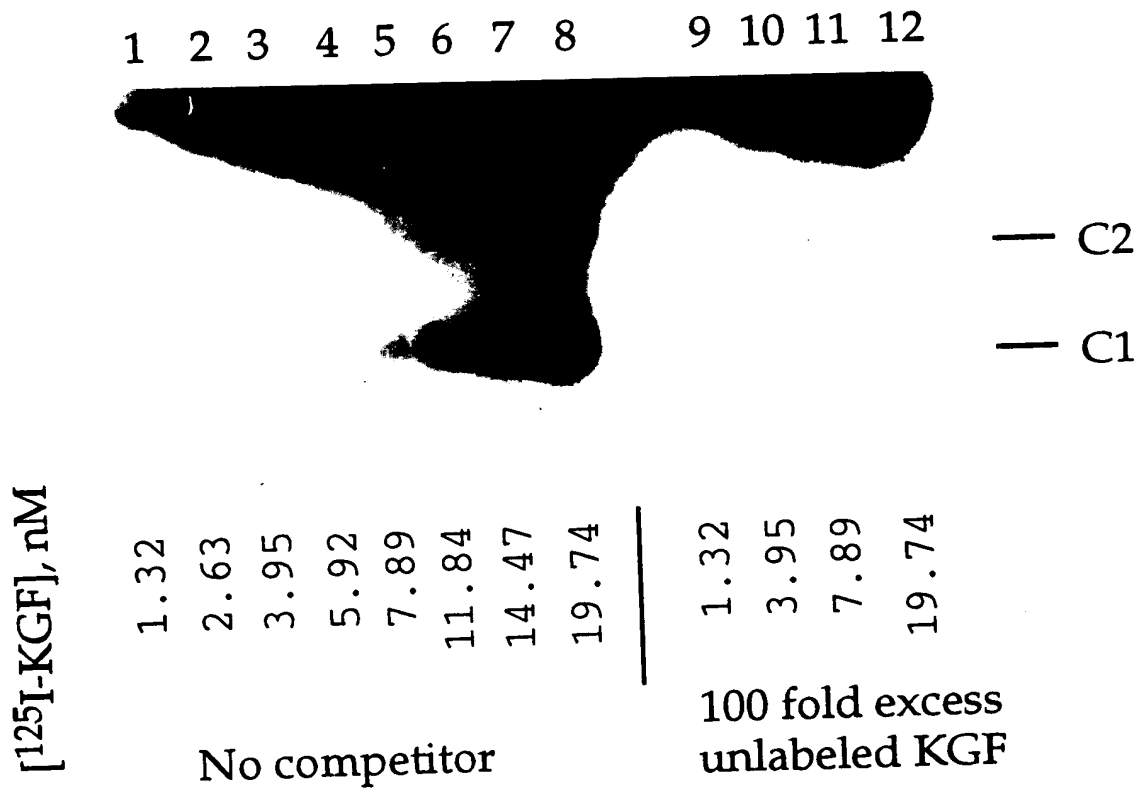


FIGURE 11

Summary Structure

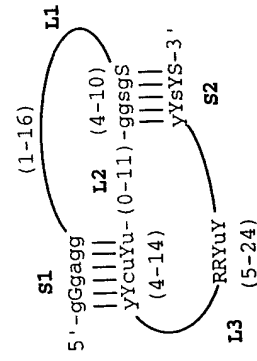


FIGURE 12A

Class 2

SEQ ID	Clone	K _d , nM	K _i , nM
230	*13F	0.03	10.0
254	*50F	0.12	
247	38F	0.33	0.2
227	10F	0.47	10.0
226	9F	0.83	
256	53F	0.7	
253	49F	1.0	
250	43F	1.13	16.7
260	57F	1.2	
248	41F	1.44	
241	27F	1.52	
235	20F	2.05	
258	55F	2.52	
261	58F	2.52	
221	3F	4.47	
236	21F	ND	
242	28F	ND	
269	Consensus		

ggacgaugcga	CACCUAGACUGUCCUCCAAGCGUGAGUUG	CUGUGCCcaga	cgacugcccg
cgaugcggUGA	UCAAUC	UUACUCUUGGCUCACC	GUGCCCcagac
ggaggacgaug	cggNGACUGAUUUUUCUUG	AUUUCUG	GUUGCCCcaga
ggaggaugcga	acgaugcggGACCAGA	UUUUUCAGCAUCCUCCCGCGC	UUUGUGUCCCG
ggaggaugcga	AUAUGGCUAGA	UCGCAUC	GUGCUUGCUUC
ggaggaugcga	gacgaugcggAUCAAA	UUCCC	UCCACGUGUUC
ggaggaugcga	ggGGACU	GCAUUGAUU	UUGAUGCCAU
ggaggaugcga	gacg	UUUCC	CGAGCCACCCG
ggaggaugcga	UGACUAUCU	CCAAUCACC	CCUGUUCUCCCG
ggaggaugcga	cggGGACUUU	CAUUGAUUUCGA	AUUAGUCCUC
ggaggaugcga	cggCAGUC	UAUUGGA	UGCUCUCCGUGCCcagacgacucg
ggaggaugcga	UUCCAGCCUGGAUUCAU	CUCCC	UGGCCcagacg
ggaggaugcga	gacgaugcggUCCGUAUAAC	UGGCCcagacg	UGGCCcagacg
ggaggaugcga	acgaugcggGAACUA	UUUCCGAACCCGCAC	GUGGCcagacg
ggaggaugcga	ggaggaugcggAUCGUAUC	CGUUCUCUCAG	CGUUGCCCCca
ggaggaugcga	augcggUCCUA	UCCUU	GUUCCCCGAGC
ggaggaugcga	cgaugcggGAUUCU	YyyYyb	syBsY
rgGrg	RsBr		

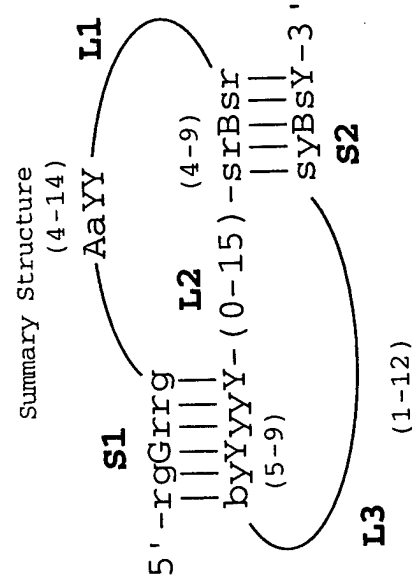


FIGURE 12B

Class 1

SEQ ID	Clone	K _d , nM	K _i , nM	
195	14N	0.4	2.0	UCCAGGGAU <u>UGAAGUGUCGGGUAGGAACA</u>
199	25N	0.9		<u>augcggcga</u> <u>GGGAUG</u> AGGAA A
191	4N	0.7	23.3	<u>augcgggUGUG</u> <u>AAAGG</u> UACCGGAA UUGC
189	1N	0.5	16.7	<u>gGAAGG ACGAUAAAG</u> AGGAA UCGAA
205	36N	8.27		<u>gga</u> <u>ggaagcggg</u> AAGGGAACA GGA
203	34N	0.8		<u>augcggcggg</u> <u>AAGAGCU</u> AAUGGA GUGGAU
207	42N	0.8	266.7	<u>augcggggag</u> <u>ACGU</u> AGACGGGAACAUAAGAACGAUCAAC
196	16N	1.4		<u>cgauccggaAGUUCUAACAAGUUGGAA</u> GGUUC
270	Consensus			<u>GGG</u> <u>aa</u> GGAA
				UAAAG
				CAACUA
				UAAAGUACCAAG
				CAACAA
				UAAAG
				CAGUC
				CAUCU
				CA CU
				YAA
				RcRR
				UGAA
				GCGGCCag
				ACAGUGC
				ACAAGUCGAACAAAG
				GGcagac
				CGAGGUGcagacgacucgcccga
				gacucgcccga
				gcccga
				acgacuc
				UGUAcaga
				gA
				CCC
				cgacucgcccga
				gacucgcccga
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Summary Structure

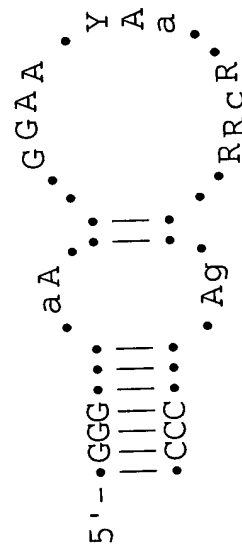


FIGURE 12C

Class 2

SEQ ID NO:	Clone	K _d , nM	K _i , nM
209	47N	1.8	
198	24N	1.2	
202	29N	0.43	13.3
204	35N	2.3	
192	6N	0.7	26.7
190	2N	0.8	66.7
211	54N	5.3	
271			Consensus

AGGAAGGUCAAGAGGAAA CAGC
 gacgaugcgg GUGGGAAGA UGAG
 AGAAGAAUGCA GGAACAGCGAAA
 ugcggGCUUAG GAAA UGGUU
 acgaugcggGC AGGGAGCAA UGAACUCAAGUACCGUGCACGU | GGGC
 GCGGA AAGGA CGAGA gggaggacgaugcggGCGGGAAGGUC
 GGG GGAAG GAUU UUGCCcagacgacucgccccga
 CGAA GACC |
 GUGcagacga cuqccccga
 AAUGUGAC ACUGCGGca
 Ccagacgac ucgccccga
 Ucagacgac ucgccccga
 agacgacuc gccccga
 AGCCCCCUGGUGGU |
 Ygay

Summary Structure

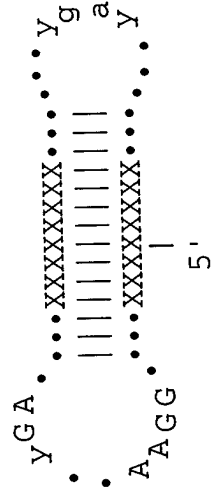


FIGURE 12D

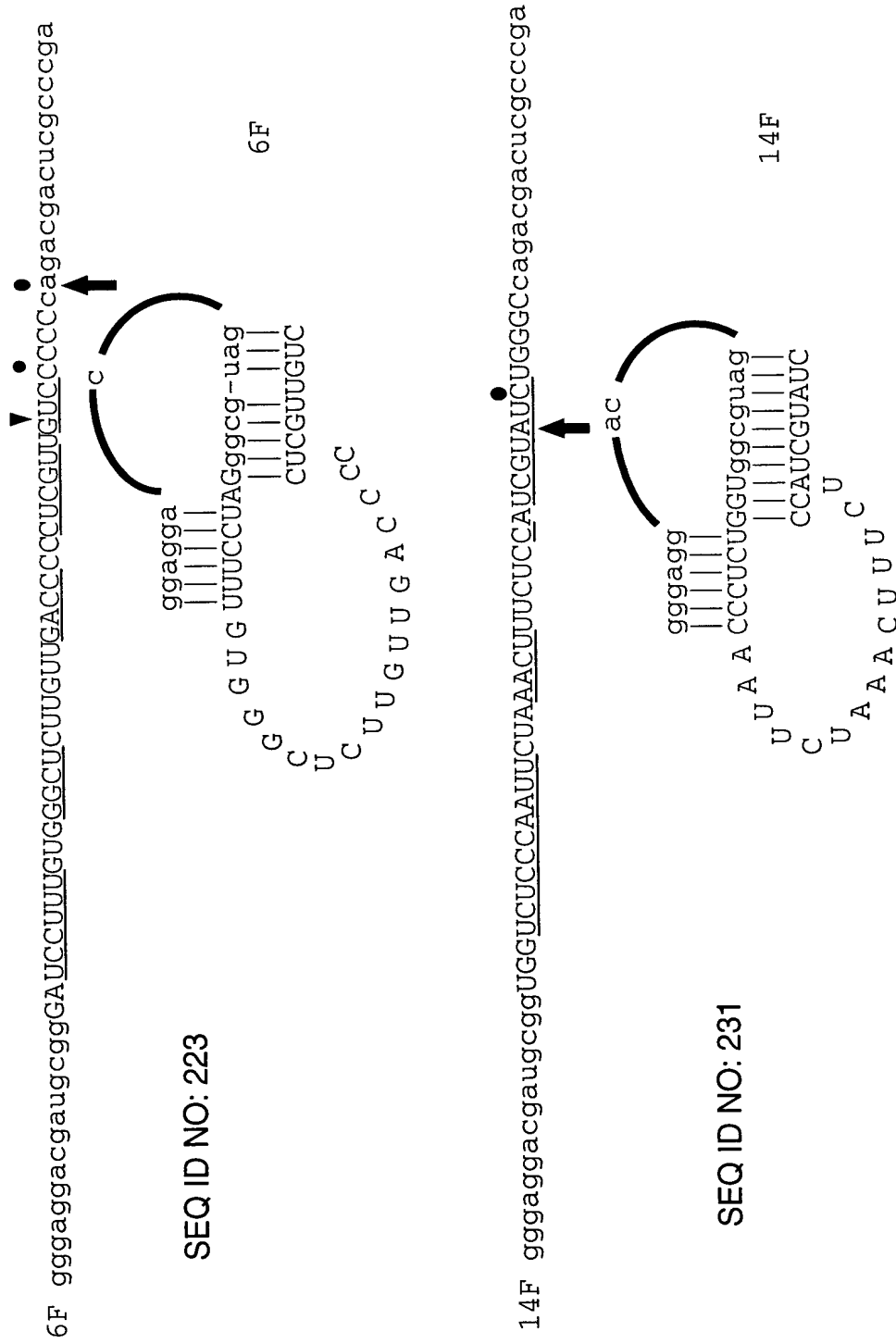


FIGURE 13